



SEQUENCE LISTING

<110> CHEN, JIA-LUN
FU, GANG
SONG, HUAI-DONG

<120> A HUMAN HSG III GENE

<130> CPA-100US

<140> 09/554,945

<141> 2000-05-22

<150> PCT/CN98/00199

<151> 1998-09-22

<160> 2

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2017

<212> DNA

<213> HOMO SAPIENS

<220> FEATURE

<221> UNSURE

<222> (1930) (1990) (2005)

<223> OTHER INFORMATION: cDNA Sequence

<400> 1

taaagctacg	ccctggccgc	agtctccgcg	tcacaggaac	ttcagcaccc	acagggcgga	60
cagcgctccc	ctctacctgg	agacttgact	cccgcgcgcc	ccaaccctgc	ttatcccttg	120
accgctcgagt	gtcagagatc	ctgcagccgc	ccagtcgccg	cccctctccc	gccccacacc	180
caccctcctg	gctcttcctg	tttttactcc	tccttttcat	tcataacaaa	agctacagct	240
ccaggagccc	agcgccgggc	tgtgacccaa	gccgagcgtg	gaagaatggg	gttcctcggg	300
accggcactt	ggattctggg	gttagtgctc	ccgattcaag	ctttccccaa	acctggagga	360
agccaagaca	aatctctaca	taatagagaa	ttaagtgcag	aaagaccttt	gaatgaacag	420
attgctgaag	cagaagaaga	caagattaaa	aaaacatatc	ctccagaaaa	caagccaggt	480
cagagcaact	attcttttgt	tgataacttg	aacctgctaa	gggcaataac	agaaaaggaa	540
aaaattgaga	aagaaaagaca	atctataaga	agctccccac	ttgataataa	gttgaatgtg	600
gaagatggtg	attcaaccaa	gaatcgaaaa	ctgatcgatg	attatgactc	tactaagagt	660
ggattggatc	ataaattttca	agatgatcca	gatggtcttc	atcaactaga	cgggactcct	720
ttaaccgctg	aagacattgt	ccataaaaatc	gctgccagga	tttatgaaga	aaatgacaga	780
gccgtgtttg	acaagattgt	ttctaaacta	cttaatctcg	gccttatcac	agaaagccaa	840
gcacatacac	tggaagatga	agtagcagag	gtttttacaaa	aattaatctc	aaaggaagcc	900
aacaattatg	aggaggatcc	caataagccc	acaagctgga	ctgagaatca	ggctggaaaa	960
ataccagaga	aagtgactcc	aatggcagca	attcaagatg	gtcttgctaa	gggagaaaac	1020
gatgaaacag	tatctaacac	attaaccttg	acaaatggct	tggaaaggag	aactaaaacc	1080
tacagtgaag	acaactttag	ggactttcaa	tattttccaa	atttctatgc	gctactgaaa	1140
agtattgatt	cagaaaaaga	agcaaaaagag	aaagaaacac	tgattactat	catgaaaaca	1200
ctgattgact	ttgtgaagat	gatggtgaaa	tatggaacaa	tatctccaga	agaaggtggt	1260
tcctaccttg	aaaacttgga	tgaaatgatt	gctcttcaga	ccaaaaacaa	gctagaaaaa	1320
aatgctactg	acaatataag	caagcttttc	ccagcaccat	cagagaagag	tcatgaagaa	1380
acagacagta	ccaaggaaga	agcagctaag	atggaaaagg	aatatggaag	cttgaaggat	1440
tccacaaaag	atgataactc	caaccaggga	ggaaagacag	atgaacccaa	aggaaaaaca	1500

RECEIVED
AUG 22 2001
TECH CENTER 1600/2900

gaagcctatt	tggaagccat	cagaaaaaat	attgaatggt	tgaagaaaca	tgacaaaaag	1560
ggaaataaag	aagattatga	cctttcaaag	atgagagact	tcatacaataa	acaagctgat	1620
gcttatgtgg	agaaaggcat	ccttgacaag	gaagaagccg	aggccatcaa	gcgcatttat	1680
agcagcctgt	aaaaatggca	aaagatccag	gagtccttca	actgtttcag	aaaacataat	1740
atagcttaaa	acacttctaa	ttctgtgatt	aaaatttttt	gacccaaggg	ttattagaaa	1800
gtgctgaatt	tacagtagtt	aacctttttac	aagtgggttaa	aacatagctt	tcttcccgtta	1860
aaaactatct	gaaagtaaag	ttgtatgtaa	gctgagattt	tgtatacagg	aatccttatt	1920
tcctcatagn	cttattattt	tataatcagg	aatatgttgc	tttggaaaaa	gcctcttaat	1980
gggctgacn	taaaaactca	atccttcttc	cactgtc			2017

<210> 2
 <211> 468
 <212> PRT
 <213> HOMO SAPIENS

<400> 2

Met	Gly	Phe	Leu	Gly	Thr	Gly	Thr	Trp	Ile	Leu	Val	Leu	Val	Leu	Pro
1			5					10						15	
Ile	Gln	Ala	Phe	Pro	Lys	Pro	Gly	Gly	Ser	Gln	Asp	Lys	Ser	Leu	His
			20					25					30		
Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln	Ile	Ala	Glu
		35					40					45			
Ala	Glu	Glu	Asp	Lys	Ile	Lys	Lys	Thr	Tyr	Pro	Pro	Glu	Asn	Lys	Pro
	50					55					60				
Gly	Gln	Ser	Asn	Tyr	Ser	Phe	Val	Asp	Asn	Leu	Asn	Leu	Leu	Arg	Ala
65					70					75					80
Ile	Thr	Glu	Lys	Glu	Lys	Ile	Glu	Lys	Glu	Arg	Gln	Ser	Ile	Arg	Ser
			85					90					95		
Ser	Pro	Leu	Asp	Asn	Lys	Leu	Asn	Val	Glu	Asp	Val	Asp	Ser	Thr	Lys
		100					105					110			
Asn	Arg	Lys	Leu	Ile	Asp	Asp	Tyr	Asp	Ser	Thr	Lys	Ser	Gly	Leu	Asp
	115					120						125			
His	Lys	Phe	Gln	Asp	Asp	Pro	Asp	Gly	Leu	His	Gln	Leu	Asp	Gly	Thr
	130					135					140				
Pro	Leu	Thr	Ala	Glu	Asp	Ile	Val	His	Lys	Ile	Ala	Ala	Arg	Ile	Tyr
145					150					155					160
Glu	Glu	Asn	Asp	Arg	Ala	Val	Phe	Asp	Lys	Ile	Val	Ser	Lys	Leu	Leu
			165						170					175	
Asn	Leu	Gly	Leu	Ile	Thr	Glu	Ser	Gln	Ala	His	Thr	Leu	Glu	Asp	Glu
		180						185				190			
Val	Ala	Glu	Val	Leu	Gln	Lys	Leu	Ile	Ser	Lys	Glu	Ala	Asn	Asn	Tyr
	195					200						205			
Glu	Glu	Asp	Pro	Asn	Lys	Pro	Thr	Ser	Trp	Thr	Glu	Asn	Gln	Ala	Gly
	210					215					220				
Lys	Ile	Pro	Glu	Lys	Val	Thr	Pro	Met	Ala	Ala	Ile	Gln	Asp	Gly	Leu
225					230					235					240
Ala	Lys	Gly	Glu	Asn	Asp	Glu	Thr	Val	Ser	Asn	Thr	Leu	Thr	Leu	Thr
			245						250					255	
Asn	Gly	Leu	Glu	Arg	Arg	Thr	Lys	Thr	Tyr	Ser	Glu	Asp	Asn	Phe	Arg
		260						265				270			
Asp	Phe	Gln	Tyr	Phe	Pro	Asn	Phe	Tyr	Ala	Leu	Leu	Lys	Ser	Ile	Asp
	275					280						285			
Ser	Glu	Lys	Glu	Ala	Lys	Glu	Lys	Glu	Thr	Leu	Ile	Thr	Ile	Met	Lys
	290					295					300				
Thr	Leu	Ile	Asp	Phe	Val	Lys	Met	Met	Val	Lys	Tyr	Gly	Thr	Ile	Ser
305					310					315					320
Pro	Glu	Glu	Gly	Val	Ser	Tyr	Leu	Glu	Asn	Leu	Asp	Glu	Met	Ile	Ala

[illegible]